* NOTICES *

1.This document has been translated by computer. So the translation may not reflect the original precisely.
2.**** shows the word which can not be translated.
3.In the drawings, any words are not translated.

CORRECTION OR AMENDMENT

[Official Gazette Type] Printing of amendment by the convention of 2 of Article 17 of patent law
[Section partition] The 1st partition of the 1st section
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[Procedure amendment 1]
[Document to be Amended] Specification
[Item(s) to be Amended] 0134
[Method of Amendment] Modification
[Proposed Amendment]
[0134] Quantitive measurement is performed at step 976. Current experimental data is compared with front experimental data as an example (the value calculated at step 975 in this case is used). As another example, the hybridization reinforcement and experimental data of RNA of known amounts (bacteria origin etc.) which exist in a living thing specimen can also be compared. Thus, it is also possible to correct the experiment to which it could also prove whether it was the right, a display, i.e., a call, of a gene expression condition, it could also correct the threshold to, and was carried out further previously.
[Procedure amendment 2]
[Document to be Amended] Specification
[Item(s) to be Amended] 0138
[Method of Amendment] Modification
[Proposed Amendment]
[0138] Drawing 22 is a screen display in which the analysis result of the selected gene is shown. The hybridization reinforcement of a perfect involution probe and a desynapsis probe in each base location of the selected gene is shown in the graphics viewing area 1032 of the screen display 1030 in the form of a bar graph. The inverse video of the selected gene is carried out to the data display field 1034.
[Procedure amendment 3]
[Document to be Amended] Specification
[Item(s) to be Amended] 0144
[Method of Amendment] Modification
[Proposed Amendment]
[0144] Drawing 25 shows the screen display showing the comparison of the experimental result about two or more selected genes. The graphics viewing area 1062 and the data display field 1064 are included in the screen display 1160. The graph of the ratio of the hybridization reinforcement of the perfect involution probe in each base location and a desynapsis probe is displayed on the graphics viewing area about each of the experiment/gene chosen in the data display field. In the suitable example, a different color for every

gene shows an experiment name, a gene name, and a data plot so that the difference between two or more selected genes may be known clearly.
[Procedure amendment 4]
[Document to be Amended] Specification
[Item(s) to be Amended] 0153
[Method of Amendment] Modification
[Proposed Amendment]
[0153] The judgment of whether (Ipm-Imm)-(Jpm-Jmm)>=DDIF and (Ipm-Imm)/(Jpm-Jmm)>=RDIF are materialized is made at step 1316. When this formula is realized, 1 **** of NDEC(s) is carried out (step 1318). Generally, NDEC is a value which shows that the possibility that the gene expression of a probe pair of an experiment specimen is smaller than the gene expression of a criteria specimen (that is, it is decreasing) is high. NDEC -- using -- a criteria specimen -- comparing -- the gene expression of an experiment specimen -- being large (that is, it increasing) -- being small (that is, it decreasing) -- or with no change -- that judgment is made.
[Procedure amendment 5]
[Document to be Amended] Specification
[Item(s) to be Amended] 0185
[Method of Amendment] Modification
[Proposed Amendment]
[0185] A system asks for change of the gene expression in two selected experiments according to the method explained by drawing 28 and drawing 29. The data generated by this comparison is shown to the data display field by the tabular format. "Experiment Name" shows the name which the user specified to comparative experiments. "Gene Name" shows the name of a gene. The numeric value of "Inc" and "Dec" shows the value of NINC and NDEC, as explained with reference to drawing 28. Specifically, "Inc" shows the number of the base locations in a gene whose difference and ratio of hybridization reinforcement of a perfect involution probe and a desynapsis probe are intentionally large in experimental data.

[Translation done.]